

ABSTRACT OF THE INVENTION

The methods and products that are described in the present patent application are designed to determine by serial analysis the transcriptional activation pathways used by any compound of interest that is biologically active in a cell. We have engineered a library of transgenic or recombinant cell lines that allow the identification of simultaneous transcriptional pathways possibly used by the compound. Each cell line constituting the library has been engineered by stable transfection thereof by retroviral integration, to carry a reporter gene under the transcriptional control of a particular transcription factor or family thereof endogenous to the host cell. This is achieved by having the expression of the reporter gene driven by a minimal promoter and a transcription factor responsive-element (TF-RE) or a tandem or concatemer thereof. In its complete form, the library contains a large collection of reporter constructs responding to individual factors, each of which can in turn be studied in a large repertory of cell lines. Such an approach provides a global view of gene transcription activation in response to diverse stimuli in multiple cellular environments and is a significant improvement over case-by-case pproaches. A compound screened against such a library provides a profile of selectivity for a given transcription factor and for a given cell type, which profile is used to select good selective putative therapeutics.